



DATE: 04/30/2001

TIME: 09:22:54

Input Set: A:\2879-US 041201 Seq List.txt
Output Set: N:\CRF3\04302001\1835147.raw

PATENT APPLICATION: US/09/835,147

(/- °

```
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      3 <110> APPLICANT: Maliszewski, Charles R.
              Gayle III, Richard B.
              Price, Virginia L.
              Gimpel, Steven D.
      8 <120> TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
     10 <130> FILE REFERENCE: 2879-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/835,147
C--> 13 <141> CURRENT FILING DATE: 2001-04-13
     15 <150> PRIOR APPLICATION NUMBER: US 60/104,585
     16 <151> PRIOR FILING DATE: 1998-10-16
     18 <150> PRIOR APPLICATION NUMBER: US 60/107,466
     19 <151> PRIOR FILING DATE: 1998-11-06
     21 <150> PRIOR APPLICATION NUMBER: US 60/149,010
     22 <151> PRIOR FILING DATE: 1999-08-13
     24 <150> PRIOR APPLICATION NUMBER: PCT/US99/22955
     25 <151> PRIOR FILING DATE: 1999-10-13
     27 <160> NUMBER OF SEQ ID NOS: 31
     29 <170> SOFTWARE: PatentIn Ver. 2.0
     31 <210> SEQ ID NO: 1
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     33 <212> TYPE: DNA
     34 < 213 > ORGANISM: Homo sapiens
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     37 <221> NAME/KEY: CDS
     38 <222> LOCATION: (67)..(1596)
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               Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser
     44
                                                    10
     45
     47 aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata
     48 Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
                                                 2.5
     49 15
                             20
     51 gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac
     52 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
                         35
                                             40
     55 gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta
     56 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
     57
                     50
                                         55
     59 tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg
     60 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
                                     70
                 65
     63 cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt
     64 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
                                 85
                                                     90
             80
     65
     67 gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa
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68 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu

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69 95 100 105 110	
71 aga get agg gaa gtg att eea agg tee eag eac eaa gag aca eee gtt	444
72 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val	
73 115 120 125	•
75 tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa	492
76 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu	
77 130 135 140	
79 gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac	540
80 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn	
81 145 150 155	
83 tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa	588
84 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu	
05 100 200	636
87 ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt	050
88 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser	
05 175	604
91 cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag	684
92 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln	
93 195 200 205	
95 gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act	732
96 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr	
97 210 215 220	
99 ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa	780
100 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln	
101 225 230 235	
103 ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg	828
104 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu	
105 240 245 250	
107 tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att	876
108 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile	
108 Cys 141 GIY Bys Rsp GII AId Bed 114 GI 126 Bed 112 Life 115 116 116 117 117 117 117 117 117 117 117	
111 cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga	924
111 Cay git god agt dat gad att the agg gat the type the tat eet ggd 112 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly	724
113	972
115 tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc	312
116 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr	
117 290 295 300	1000
119 aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt	1020
120 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly	
121 305 310 315	
123 att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac	1068
124 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn	
125 320 325 330	
125 320 325 330 127 acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg	1116
125 320 325 330 127 acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg	1116
125 320 325 330 127 acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 128 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu	1116
125 320 325 330 127 acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 128 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu 129 335 340 345 350	1116 1164
125 320 325 330  127 acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg  128 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu  129 335 340 345 350  131 cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg	
125 320 325 330 127 acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 128 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu 129 335 340 345 350	

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Output Set: N:\CRF3\04302001\I835147.raw

									•		•						
13'	atg	aaσ	t.t.t.	t.ta	aac	tta	aca	tca	qaq	aaa	qtc	tct	cag	gaa	aag	gtg	1212
13	Met	Lvs	Phe	Leu	Asn	Leu	Thr	Ser	Ğlu	Lys	val	Ser	Gln	Glu	Lys	Val	
13				370					375					380			
13	act	gag	atg	atg	aaa	aag	ttc	tgt	gct	cag	cct	tgg	gag	gag	ata	aaa	1260
14	Thr	Glu	Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	
14			385		-	_		390					395				
14	aca	tct	tac	gct	gga	gta	aag	gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	1308
14	Thr	Ser	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	
14	5	400					405					410					
14	tct,	ggt	acc	tac	att	ctc	tcc	ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	1356
14	3 Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	$\mathtt{Tyr}$	His	Phe	Thr	
14	415					420					425					430	
15	L gct	gat	tcc	tgg	gag	cac	atc	cat	ttc	att	ggc	aag	atc	cag	ggc	agc	1404
15	2 Åla	Asp	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	
15					435					440					445		
15	5 gac	gcc	ggc	tgg	act	ttg	ggc	tac	atg	ctg	aac	ctg	acc	aac	atg	atc	1452
15	á Asp	Ala	Gly	Trp	Thr	Leu	Gly	Tyr		Leu	Asn	Leu	Thr		Met	Ile	
15				450					455					460			
15	cca	gct	gag	caa	cca	ttg	tcc	aca	cct	ctc	tcc	cac	tcc	acc	tat	gtc	1500
16	) Pro	Ala	Glu	Gln	Pro	Leu	Ser		Pro	Leu	Ser	His		Thr	Tyr	Val	
16			465					470					475				2540
16	ttc	ctc	atg	gtt	cta	ttc	tcc	ctg	gtc	ctt	ttc	aca	gtg	gcc	atc	ata	1548
16	l Phe	Leu	Met	Val	Leu	Phe	Ser	Leu	Val	Leu	Phe		Val	Ala	Ile	He	
16		480					485					490					1506
16	7 ggc	ttg	ctt	atc	ttt	cac	aag	cct	tca	tat	ttc	tgg	aaa	gat	atg	gta	1596
	3 Gly		Leu	Ile	Phe		Lys	Pro	Ser	Tyr		Trp	Lys	Asp	мет	Val	
	9 495					500					505					510	1599
	L tag	_			_												1333
	4 <21																
	5 <21				10												
	5 <21							_									
	7 <21					o sa	piens	5									
1/	9 < 40	0> 5	EQUE:	NCE:	∠ T	<i>α</i> 1	Com	A an	17 o 1	Twa	mh r	Dho	Care	Sar	T.37 C	Δen	
	Met	GLU	Asp	THE	ьуs 5	GIU	ser	ASII	Val	10	1111	FILE	Cys	Der	15	ASII	
18	l 1 3 Ile	T 011	717	т10	-	Clar	Dho	cor	Car		Tla	ΔΊа	Va l	Tle		Len	
		теп	Ата	20	ьеu	GIY	rne	361	25	110	110	niu	, ,	30	1114	Lou	
18	6 Leu	712	Wa l		LON	Thr	Gln	λen		Δla	T.e.ii	Pro	Glu		Val	Lvs	
18		ніа	35	GLY	пец	1111	GIII	40	цуз	2114	Deu	110	45	11211	,	-1-	
	, 9 Tyr	Glv		Val	T.011	Asn	Δla		Ser	Ser	His	Thr		Leu	Tvr	Ile	
19		50	110	Val	пси	115P	55	G.L.J	001	002		60			- 4		
	Z Tyr		Tro	Pro	Δla	Glu		Glu	Asn	Asp	Thr	Glv	Val	Val	His	Gln	
19		טענג	112	110	liiu	70	ביים				75	1				80	
	5 Val	Glu	Glu	Cvs	Ara		Lvs	Glv	Pro	Glv	Ile	Ser	Lys	Phe	Val	Gln	
19				-10	85			1		90	ĺ		•		95		
	3 B Lys	Va1	Asn	Glu		Glv	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	
19				100		-1		•	105		•	-		110	_		
	l Arg	Glu	Val		Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	
20			115			_		120					125				

1650 - L

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/835,147

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204 205	Gly	Ala 130	Thr	Ala	Gly	Met	Arg 135	Leu	Leu	Arg	Met	Glu 140	Ser	Glu	Glu	Leu
207	Ala 145		Arg	Val	Leu	Asp 150		Val	Glu	Arg	Ser 155	Leu	Ser	Asn	Tyr	Pro 160
210 211	Phe	Asp	Phe	Gln	Gly 165		Arg	Ile	Ile	Thr 170	Gly	Gln	Glu	Glu	Gly 175	Ala
213 214	Tyr	Gly	Trp	Ile 180		Ile	Asn	Tyr	Leu 185	Leu	Gly	Lys	Phe	Ser 190	Gln	Lys
216 217	Thr	Arg	Trp 195	Phe	Ser	Ile	Val	Pro 200	Tyr	Glu	Thr	Asn	Asn 205	Gln	Glu	Thr
219 220	Phe	Gly 210	Ala	Leu	Asp	Leu	Gly 215	Gly	Ala	Ser	Thr	Gln 220	Val	Thr	Phe	Val
223	225					230					Asn 235					240
226					245					250	His				255	
229				260					265		Ala			270		
232			275					280			Phe		285			
235		290					295				Thr	300				
238	305					310					Glu 315					320
241					325					330	Glu				335	
244				340					345		Gly			350		
247			355					360			Phe		365			
250		370					375				Gln	380				
253	385					390					Glu 395					400
256					405					410	Glu				415	
259				420					425		Tyr			430		
262		_	435					440			Ile		445			
265		450					455				Thr	460				
268	465					470					Ser 475					480
271					485					490					Gly 495	Leu
273 274	Leu	Ile	Phe	His 500	Lys	Pro	Ser	Tyr	Phe 505	Trp	Lys	Asp	Met	Val 510		
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278 <211> LENGTH: 476
279 <212> TYPE: PRT
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion
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290 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
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                                     25
293 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
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296 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
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299 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
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302 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
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305 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
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               100
308 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
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                                120
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311 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
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        130
312
314 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
                                            155
315 145
                        150
317 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Gly Ala
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                                        170
320 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
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321
                180
323 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
                                200
           195
326 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
                                                220
        210
                            215
329 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
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                                            235
332 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
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                                                            255
                    245
335 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
                                    265
                260
338 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
                                280
                                                    285
            275
341 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
                            295
                                                300
344 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
                                           315
                      310
345 305
347 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
348
                    325
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in th <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/835,147

DATE: 04/30/2001

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L:12 M:270 C: Current Application Number differs, Replaced Application Number L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4